

M. Pak

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/352,570

DATE: 11/22/2000

TIME: 11:33:59

Input Set : A:\00398.506001.SEQLIST.TXT

Output Set: N:\CRF3\11222000\I352570.raw

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4 <110> APPLICANT: Michael E. Mendelsohn
7 <120> TITLE OF INVENTION: METHOD FOR ASSAYING COMPOUNDS AFFECTING
8 CELL DIVISION
10 <130> FILE REFERENCE: 00398/506001
12 <140> CURRENT APPLICATION NUMBER: 09/352,570
13 <141> CURRENT FILING DATE: 1999-07-13
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 618
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)...(618)
28 <400> SEQUENCE: 1
29 atg gcg ctg cag ctc tcc cyg gag cag gga atc acc ctg cgc ggg agc 48
30 Met Ala Leu Gln Leu Ser Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser
31 1 5 10 15
33 gcc gaa atc gtg gcc gag ttc ttc tca ttc ggc atc aac agc att tta 96
34 Ala Glu Ile Val Ala Glu Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu
35 20 25 30
37 tat cag cgt gcc ata tat cca tct gaa acc ttt act cga gtg cag aaa 144
38 Tyr Gln Arg Gly Ile Tyr Pro Ser Glu Thr Phe Thr Arg Val Gln Lys
39 35 40 45
41 tac gga ctc acc ttg ctt gta act act gat ctt gag ctc ata aaa tac 192
42 Tyr Gly Leu Thr Leu Leu Val Thr Thr Asp Leu Glu Leu Ile Lys Tyr
43 50 55 60
45 cta aat aat gtg gtg gaa caa ctg aaa gat tgg tta tac aag tgt tca 240
46 Leu Asn Asn Val Val Glu Gln Leu Lys Asp Trp Leu Tyr Lys Cys Ser
47 65 70 75 80
49 gtt cag aaa ctg gtt gta gtt atc tca aat att gaa agt ggt gag gtc 288
50 Val Gln Lys Leu Val Val Val Ile Ser Asn Ile Glu Ser Gly Glu Val
51 85 90 95
53 ctg gaa aga tgg cag ttt gat att gag tgt gac aag act gca aaa gat 336
54 Leu Glu Arg Trp Gln Phe Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp
55 100 105 110
57 gac agt gca ccc aga gaa aag tct cag aaa gct atc cag gat gaa atc 384
58 Asp Ser Ala Pro Arg Glu Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile
59 115 120 125
61 cgt tca gtg atc aga cag atc aca gct acg gtg aca ttt ctg cca ctg 432
62 Arg Ser Val Ile Arg Gln Ile Thr Ala Thr Val Thr Phe Leu Pro Leu
63 130 135 140
65 ttg gaa gtt tct tgt tca ttt gat ctg ctg att tat aca gac aaa gat 480
66 Leu Glu Val Ser Cys Ser Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp
67 145 150 155 160
69 ttg gtt gta cct gaa aaa tgg gaa gag tcg gga cca cag ttt att acc 528
```

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70 Leu Val Val Pro Glu Lys Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr
71                165                170                175
73 aat tct gag gaa gtg cgc ctt cgt tca ttt act act.aca atc cac aaa   576
74 Asn Ser Glu Glu Val Arg Leu Arg Ser Phe Thr Thr Thr Ile His Lys
75                180                185                190
77 gta aat agc atg gtg gcc tac aaa att cct gtc aat gac tga           618
78 Val Asn Ser Met Val Ala Tyr Lys Ile Pro Val Asn Asp *
79                195                200                205

83 <210> SEQ ID NO: 2
84 <211> LENGTH: 199
85 <212> TYPE: PRT
86 <213> ORGANISM: Homo sapiens
88 <400> SEQUENCE: 2
89 Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser Ala Glu Ile Val Ala Glu
90 1      5      10      15
91 Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu Tyr Gln Arg Gly Ile Tyr
92      20      25      30
93 Pro Ser Glu Thr Phe Thr Arg Val Gln Lys Tyr Gly Leu Thr Leu Leu
94      35      40      45
95 Val Thr Thr Asp Leu Glu Leu Ile Lys Tyr Leu Asn Asn Val Val Glu
96      50      55      60
97 Gln Leu Lys Asp Trp Leu Tyr Lys Cys Ser Val Gln Lys Leu Val Val
98 65      70      75      80
99 Val Ile Ser Asn Ile Glu Ser Gly Glu Val Leu Glu Arg Trp Gln Phe
100      85      90      95
101 Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp Asp Ser Ala Pro Arg Glu
102      100     105     110
103 Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile Arg Ser Val Ile Arg Gln
104      115     120     125
105 Ile Thr Ala Thr Val Thr Phe Leu Pro Leu Leu Glu Val Ser Cys Ser
106      130     135     140
107 Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp Leu Val Val Pro Glu Lys
108 145     150     155     160
109 Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr Asn Ser Glu Glu Val Arg
110      165     170     175
111 Leu Arg Ser Phe Thr Thr Thr Ile His Lys Val Asn Ser Met Val Ala
112      180     185     190
113 Tyr Lys Ile Pro Val Asn Asp
114      195

117 <210> SEQ ID NO: 3
118 <211> LENGTH: 600
119 <212> TYPE: DNA
120 <213> ORGANISM: Ovis aries
122 <220> FEATURE:
123 <221> NAME/KEY: CDS
124 <222> LOCATION: (1)...(600)
126 <400> SEQUENCE: 3
127 cgg gag caa ggc atc acc ttg cgc ggg agc gcc gag atc gtg gcc gag   48
128 Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser Ala Glu Ile Val Ala Glu

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129 1          5          10          15
131 ttc ttc tca ttt ggt atc aac agt att tta tat cag cgt ggc ala tat 96
132 Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu Tyr Gln Arg Gly Ile Tyr
133          20          25          30
135 cca tcg gaa acc ttt act cga gtg cag aaa tat gga ctc acc ttg ctt 144
136 Pro Ser Glu Thr Phe Thr Arg Val Gln Lys Tyr Gly Leu Thr Leu Leu
137          35          40          45
139 gta act act gat cct gag ctc ata aaa tac cta aat aat gtg gtg gat 192
140 Val Thr Thr Asp Pro Glu Leu Ile Lys Tyr Leu Asn Asn Val Val Asp
141          50          55          60
143 caa cta aaa gaa tgg tta tac aag tgt tca gtt cag aaa ctg gtg gta 240
144 Gln Leu Lys Glu Trp Leu Tyr Lys Cys Ser Val Gln Lys Leu Val Val
145 65          70          75          80
147 gtc atc tca aat att gaa agt gga gag gtc ctt gaa aga tgg caa ttt 288
148 Val Ile Ser Asn Ile Glu Ser Gly Glu Val Leu Glu Arg Trp Gln Phe
149          85          90          95
151 gat att gag tgt gac aag act gca aaa gat gac agt gca ccc aga gaa 336
152 Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp Asp Ser Ala Pro Arg Glu
153          100          105          110
155 aag tct cag aaa gct atc caa gat gaa atc cgt tca gtg atc aga cag 384
156 Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile Arg Ser Val Ile Arg Gln
157          115          120          125
159 atc aca gct aca gta aca ttt ctg cca ctg ttg gaa gtt tct tgt tca 432
160 Ile Thr Ala Thr Val Thr Phe Leu Pro Leu Leu Glu Val Ser Cys Ser
161          130          135          140
163 ttt gat ctc ctc att tat aca gac aaa gat ctg gtt gta cct gag aaa 480
164 Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp Leu Val Val Pro Glu Lys
165 145          150          155          160
167 tgg gaa gag tcc gga cca cag ttc att acc aat tct gaa gaa gtt cgt 528
168 Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr Asn Ser Glu Glu Val Arg
169          165          170          175
171 ctt cgt tca ttc act act aca att cac aaa gta aat agc atg gta gcc 576
172 Leu Arg Ser Phe Thr Thr Thr Ile His Lys Val Asn Ser Met Val Ala
173          180          185          190
175 tac aaa att cct gtc cat gac tga 600
176 Tyr Lys Ile Pro Val His Asp *
177          195
180 <210> SEQ ID NO: 4
181 <211> LENGTH: 199
182 <212> TYPE: PRT
183 <213> ORGANISM: Ovis aries
185 <400> SEQUENCE: 4
186 Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser Ala Glu Ile Val Ala Glu
187 1          5          10          15
188 Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu Tyr Gln Arg Gly Ile Tyr
189          20          25          30
190 Pro Ser Glu Thr Phe Thr Arg Val Gln Lys Tyr Gly Leu Thr Leu Leu
191          35          40          45
192 Val Thr Thr Asp Pro Glu Leu Ile Lys Tyr Leu Asn Asn Val Val Asp

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193      50      55      60
194 Gln Leu Lys Glu Trp Leu Tyr Lys Cys Ser Val Gln Lys Leu Val Val
195 65      70      75      80
196 Val Ile Ser Asn Ile Glu Ser Gly Glu Val Leu Glu Arg Trp Gln Phe
197      85      90      95
198 Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp Asp Ser Ala Pro Arg Glu
199      100      105      110
200 Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile Arg Ser Val Ile Arg Gln
201      115      120      125
202 Ile Thr Ala Thr Val Thr Phe Leu Pro Leu Leu Glu Val Ser Cys Ser
203      130      135      140
204 Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp Leu Val Val Pro Glu Lys
205 145      150      155      160
206 Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr Asn Ser Glu Glu Val Arg
207      165      170      175
208 Leu Arg Ser Phe Thr Thr Thr Ile His Lys Val Asn Ser Met Val Ala
209      180      185      190
210 Tyr Lys Ile Pro Val His Asp
211      195

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